

CLAIMS

1. Probe consisting of at least about 15 nucleotides of the transcribed spacer region between the 16S and 23S rRNA genes of prokaryotic organisms, and more particularly bacteria, and preferably from about 15 nucleotides to about the maximum number of nucleotides of the spacer region and more preferably from about 15 to about 100 nucleotides.

2. Probe according to claim 1, for use in a hybridization assay, liable to be obtained in the process which comprises constructing an oligonucleotide that is sufficiently complementary to hybridize to a sequence of the spacer region between rRNA genes, particularly the spacer region between the 16S rRNA gene and the 23S rRNA gene, selected to be unique to non-viral organisms, particularly prokaryotic organisms, more particularly bacteria, sought to be detected, with said sequence of the spacer region between rRNA genes being selected

- either by

- * comparing the nucleotide sequence of the spacer region between the rRNA genes of the sought organism with the nucleotide sequence of the spacer region between the rRNA genes of the closest neighbours,
- * selecting a sequence of at least 15 nucleotides, and preferably from about 15 to about the maximum number of nucleotides of the spacer region, and more preferably from about 15 to about 100 nucleotides of the spacer region between rRNA genes of the sought organism which presents at least one mismatch with the spacer region between the rRNA genes of at least one of the closest neighbours,

- or by

- * deleting, in the spacer region between the rRNA genes of the organism to be sought, the tRNA genes and possibly the signal sequences, to obtain a shortened spacer region and
- * determining by trial and error a specific nucleotide sequence of at least about 15 nucleotides, and preferably from about 15 to about the maximum number of nucleotides of the spacer region, and more preferably from about 15 to about 100 nucleotides, from the shortened spacer region, said sequence being able to hybridize specifically with the nucleic acids (DNA and/or RNAs) of the sought organism.

3. Probe according to anyone of claims 1 or 2, containing

- either a sequence belonging to a nucleic acid selected from the following group of nucleic acids and which includes from 15 to the maximum number of nucleotides of the selected nucleic acid:

Group NGI1:

CGATGCGTCG TTATTCTACT TCGC	NGI1
GCGAAGTAGA ATAACGACGC ATCG	NGI1IC
GCGAAGUAGA AUAAACGACGC AUCG	NGI1ICR
CGAUGCGUCG UUAUUCUACU UCGC	NGI1R

Group NGI2:

TTCGTTTACG TACCCGTTGA CTAAGTAAGC AAAC	NGI2
GTTTGCTTAC TTAGTCAACG GGTAGGTAAA CGAA	NGI2IC
GUUUGCUUAC UUAGUCAACG GGUAGGUAAA CGAA	NGI2ICR
UUGGUUUUACC UACCCGUUGA CUAAGUAAGC AAAC	NGI2R

Group NMII:

GGTCAAGTGT GACGTCGCC TG	NMII1
CAGGGCGACG TCACACTTGA CC	NMII1IC

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CAGGGCGACG UCACACUUGA CC
 GGUCAAGUGU GACGUCGCCCG UG

NMI1ICR
 NMI1R

Group NMI2:

GTTCTTGGTC AAGTGTGACG TC
 GACGTCACAC TTGACCAAGA AC
 GACGUCACAC UUGACCAAGA AC
 GUUCUUGGUC AAGUGUGACG UC

NMI2
 NMI2IC
 NMI2ICR
 NMI2R

Group NMI3:

GCGTTCGTTA TAGCTATCTA CTGTGC
 GCACAGTAGA TAGCTATAAC GAACGC
 GCACAGUAGA UAGCUAUAAAC GAACGC
 GCGUUCGUUA UAGCUAUCUA CUGUGC

NMI3
 NMI3IC
 NMI3ICR
 NMI3R

Group NMI4:

TGCGTTCGAT ATTGCTATCT ACTGTGCA
 TGCACAGTAG ATAGCAATAT CGAACGCA
 UGCACAGUAG AUAGCAAUAU CGAACGCA
 UGCGUUCGAU AUUGCUAUCU ACUGUGCA

NMI4
 NMI4IC
 NMI4ICR
 NMI4R

Group NMI5:

TTTTGTTCTTGGTCAAGTGTGACGTCGCCCTGAATGGATTCTGTTCCATT
 NMIS
 AATGGAACAGAACATCCATTCAAGGGCGACGTACACTTGACCAAGAACAAAA
 NMIS
 AAUGGAACAGAAUCCAUUCAGGGCGACGUACACUUGACCAAGAACAAAA
 NMISICR
 UUUUGUUCUUGGUCAAGUGUGACGUUCGCCUGAAUGGAUUCUGUUCCAUU
 NMISR

Group NMI6

TTTGCCTAAC ATTCCGTTGA CTAGAACATC AGAC
 GTCTGATGTT CTAGTCAACG GAATGTTAGG CAAA
 GUCUGAUGUU CUAGUCAACG GAAUGUUAGG CAAA
 UUUGCCUAAC AUUCCGUUGA CUAGAACAUAGAC

NMI6
 NMI6IC
 NMI6ICR
 NMI6R

Group HDI1:

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TTATTATGCG CGAGGCATAT TG	HDII
CAATATGCCT CGCGCATAAT AA	HDIIIC
CAAUAUGCCU CGCGCAUAAU AA	HDIIICR
UUAAUAUGCG CGAGGCAUAAU UG	HDII1R
 Group BCII:	
TTAAACATCT TACCAAAG	BCII
CTTGGTAAG ATGTTAA	BCIIIC
CUUUGGUAAG AUGUUUAA	BCIIICR
UUAAACAUUCU UACCAAAG	BCII1R
 Group BCII2:	
TTGATGTTA AACTTGCTTG GTGGA	BCI2
TCCACCAAGC AAGTTTAAAC ATCAA	BCI2IC
UCCACCAAGC AAGUUUAAAC AUCAA	BCI2ICR
UUGAUGUUUA AACUUGCUUG GUGGA	BCI2R
 Group BPI1:	
CCACACCCAT CCTCTGGACA GGCTT	BPI1
AAGCCTGTCC AGAGGATGGG TGTGG	BPI1IC
AAGCCUGUCC AGAGGAUGGG UGUGG	BPI1ICR
CCACACCCAU CCUCUGGACA GGCUU	BPI1R
 Group HII1:	
ACGCATCAAA TTGACCGCAC TT	HII1
AAAGTGCAGTC AATTGATGC GT	HII1IC
AAGUGGGUC AAUUUGAUGC GU	HII1ICR
ACGCAUCAAA UUGACCGCAC UU	HII1R
 Group HII2:	
ACTTTGAAGT GAAAACCAA AG	HII2
CTTTAAGTTT TCACCTCAAA GT	HII2IC
CUUUAAGUUU UCACUUCAAA GU	HII2ICR
ACUUUGAAGU GAAAACUUAA AG	HII2R
 Group SAI1:	
AATCGAAAGG TTCAAATTGT T	SAI1
AACAATTGGA ACCTTTCGAT T	SAI1IC

AACAAUUUGA ACCUUUCGAU U SAI1ICR
 AAUCGAAAGG UUCAAAUUGU U SAI1R

Group SAI2:

GGAAACCTGC CATTGCGTC TT SAI2
 AAGACGCAAA TGGCAGGTTT CC SAI2IC
 AAGACGCAAA UGGCAGGUUU CC SAI2ICR
 GGAAACCUGC CAUUUGCGUC UU SAI2R

Group SAI3:

TCCACGATCT AGAAATAGAT TGTAGAA SAI3
 TTCTACAATC TATTTCTAGA TCGTGGA SAI3IC
 UUCUACAAUC UAUUUCUAGA UCGUGGA SAI3ICR
 UCCACGAUCU AGAAAAGAU UGUAGAA SAI3R

Group SAI4:

TCTAGTTTA AAGAAACTAG GTT SAI4
 AACCTAGTTT CTTTAAAAC AGA SAI4IC
 AACCUAGUUU CUUUAAAACU AGA SAI4ICR
 UCUAGUUUU AAGAAACUAG GUU SAI4R

Group SPI1:

GTGAGAGATC ACCAAGTAAT GCA SPI1
 TGCATTACTT GGTGATCTCT CAC SPI1IC
 UGCAUUACUU GGUGAUCUCU CAC SPI1ICR
 GUGAGAGAUC ACCAAGUAAU GCA SPI1R

Group SPI2

AGGAACTGCG CATTGGTCTT SPI2
 AAGACCAATG CGCAGTTCCCT SPI2IC
 AAGACCAAUG CGCAGUUCCU SPI2ICR
 AGGAACUGCG CAUUGGUCUU SPI2R

Group SPI3

GAGTTTATGA CTGAAAGGTC AGAA SPI3
 TTCTGACCTT TCAGTCATAA ACTC SPI3IC
 UUCUGACCUU UCAGUCAUAA ACUC SPI3ICR
 GAGUUUAUGA CUGAAAGGUC AGAA SPI3R

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- or a variant sequence which distinguishes of any of the preceding sequences:
 - * either by addition to or removal from any of their respective extremities of one or several nucleotides;
 - * or changing within any of said sequences of one or more nucleotides;
 - * or both;

yet provided that in any of the above circumstances said probe still hybridizes with the same RNA or DNA target as the corresponding unmodified sequence.

4. Probe for detecting one or more Neisseria gonorrhoeae strains, containing:

- either a sequence belonging to a nucleic acid selected from the following groups of nucleic acids and which includes from 15 to the maximum number of nucleotides of the selected nucleic acid:

Group NGI1:

CGATGCCGTCG TTATTCTACT TCGC	NGI1
GCAGAGTAGA ATAACGACGC ATCG	NGI1IC
GCGAAGUAGA AUAAACGACGC AUCG	NGI1ICR
CGAUGCGUCG UUAUUCUACU UCGC	NGI1R

Group NGI2:

TTCGTTTACC TACCCGTTGA CTAAGTAAGC AAAC	NGI2
GTTCGCTTAC TTAGTCAACG GGTAGGTAAA CGAA	NGI2IC
GUUUGCUUAC UUAGUCAACG GGUAGGUAAA CGAA	NGI2ICR
UUGGUUUUACC UACCCGUUGA CUAAGUAAGC AAAC	NGI2R

- or a variant sequence which distinguishes of any of the preceding sequences:
 - * either by addition to or removal from any of their respective extremities of one or several nucleotides;

- * or changing within any of said sequences of one or more nucleotides;
- * or both;

yet provided that in any of the above circumstances said probe still hybridizes with the same RNA or DNA target as the corresponding unmodified sequence.

5. Process for detecting Neisseria gonorrhoeae strains in a biological sample, wherein said process comprises contacting said biological sample - in which the nucleic acids (DNAs and/or RNAs) of the strains have been made accessible to hybridization, if need be, under suitable denaturation conditions, with said nucleic acid to be detected being possibly amplified using the polymerase chain reaction, with two primers, more preferably two more evolutionarily conserved primers, flanking the target sequence of the probe - with a probe according to any of the probes of claim 4 under conditions enabling hybridization between the probe and complementary nucleic acids of the Neisseria gonorrhoeae strains, which may be present in the sample, and detecting the hybrids possibly formed, particularly with a probe hybridizing to both DNA and RNA of a Neisseria gonorrhoeae strain which may be present in the biological sample.

6. Process for detecting Neisseria gonorrhoeae, in a biological sample, according to claim 5, wherein: the hybridization medium contains about 3 x SSC, (SSC = 0.15 M NaCl, 0.015 M sodium citrate, pH 7.0) about 25 mM of phosphate buffer pH 7.1, 20% deionized formamide, 0.02% Ficoll, 0.02% bovine serum albumin, 0.02% polyvinylpyrrolidone, and about 0.1 mg/ml sheared, denatured salmon sperm DNA,
and/or
the wash medium contains about 3 x SSC, 25 mM phosphate buffer pH 7.1, and 20% deionized formamide and wherein the probe used is any of the probes of claim 4, the

hybridization temperatur being suitably adjusted to the range of ab ut 50°C and/or the wash temperature to the rang of about 50°C, and particularly wherein said target sequence and the corresponding relevant hybridization temperature (HT) and wash temperature (WT), respectively, are as follows:

GCGAAGTAGA ATAACGACGC ATCG

HT and/or WT: 50 °C.

GUUUGCUUAC UUAGUCAACG GGUAGGUAAA CGAA

HT and/or WT: 50 °C.

7. Kit for the detection in vitro of a large number, preferably all Neisseria gonorrhoeae strains in a biological sample, with said kit containing:

either

- at least one probe selected among any of those according to claim 4;
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a large number, preferably all strains of Neisseria gonorrhoeae to be carried out;
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least two probes, targeting the same nucleic acid molecule, and of which at least one is specific for Neisseria gonorrhoeae and which is selected from any one of the probes of claim 4,
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Neisseria gonorrhoeae to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least one probe selected among any of those according to claim 4, which is fixed to a solid support,
- the primers needed for performing enzymatic amplification of the DNA and/or RNA containing the target sequence of the above-mentioned probe, when appropriate,
- the buffers or components necessary for producing the buffers enabling enzymatical amplification and/or enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Neisseria gonorrhoeae to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate.

8. Probe for detecting one or more Neisseria meningitidis strains, containing:

- either a sequence belonging to a nucleic acid selected from the following group of nucleic acids and which includes from 15 to the maximum number of nucleotides of the selected nucleic acid:

Group NMI1:

GGTCAAGTGT GACGTCGCC	TG	NMI1
CAGGGCGACG TCACACTTGA CC		NMI1IC
CAGGGCGACG UCACACUUGA CC		NMI1ICR
GGUCAAGUGU GACGUCGCC	UG	NMI1R

Group NMI2:

GTTCTTGGTC AAGTGTGACG TC	NMI2
GACGTCACAC TTGACCAAGA AC	NMI2IC
GACGUCACAC UUGACCAAGA AC	NMI2ICR
GUUCUUGGUC AAGUGUGACG UC	NMI2R

Group NMI3:

GCGTTCGTTA TAGCTATCTA CTGTGC	NMI3
GCACAGTAGA TAGCTATAAC GAACGC	NMI3IC
GCACAGUAGA UAGCUAUAC GAACGC	NMI3ICR

GCGUUCGUUA UAGCUAUCUA CUGUGC

NMI3R

Group NMI4:

TGCGTTCGAT ATTGCTATCT ACTGTGCA	NMI4
TGCACAGTAG ATAGCAATAT CGAACGCA	NMI4IC
UGCACAGUAG AUAGCAAUAU CGAACGCA	NMI4ICR
UGCGUUCGAU AUUGCUALCU ACUGUGCA	NMI4R

Group NMI5:

TTTTGTTCTTGGTCAAGTGTGACGTCGCCCTGAATGGATTCTGTTCCATT	NMI5
AATGGAACAGAACATCCATTAGGGCGACGTCACACTTGACCAAGAACAAAA	NMI5C
AAUGGAAACAGAAUCCAUUCAGGGCGACGUACACUUGACCAAGAACAAAA	NMI5ICR
UUUJUGUUCUUGGUCAAGUGUGACGUCCUGAAUGGAUUCUGUCCAUU	NMI5R

Group NMI6:

TTTGCCTAAC ATTCCGTTGA CTAGAACATC AGAC	NMI6
GTCTGATGTT CTAGTCAACG GAATGTTAGG CAAA	NMI6IC
GUCUGAUGUU CUAGUCAACG GAAUGUUAGG CAAA	NMI6ICR
UUUGCCUAAC AUUCCGUUGA CUAGAACAUU AGAC	NMI6R

- or a variant sequence which distinguishes of any of the preceding sequences:

- * either by addition to or removal from any of their respective extremities of one or several nucleotides;
- * or changing within any of said sequences of one or more nucleotides;
- * or both;

yet provided that in any of the above circumstances said probe still hybridizes with the same RNA or DNA target as the corresponding unmodified sequence.

9. Process for detecting Neisseria meningitidis strains in a biological sample, wherein said process

comprises contacting said biological sample - in which the nucleic acids (DNAs and/or RNAs) of the strains have been made accessible to hybridization, if need be, under suitable denaturation conditions, with said nucleic acid to be detected being possibly amplified using the polymerase chain reaction, with two primers, more preferably two more evolutionarily conserved primers, flanking the target sequence of the probe - with a probe according to any one of claim 8 under conditions enabling hybridization between the probe and complementary nucleic acids of the *Neisseria meningitidis* strains, which may be present in the sample, and detecting the hybrids possibly formed particularly with a probe hybridizing to both DNA and RNA of a *Neisseria meningitidis* strain which may be present in the biological sample.

10. Process for detecting *Neisseria meningitidis*, in a biological sample, according to claim 9, wherein: the hybridization medium contains about 3 x SSC, (SSC = 0.15 M NaCl, 0.015 M sodium citrate, pH 7.0) about 25 mM of phosphate buffer pH 7.1, 20% deionized formamide, 0.02% Ficoll, 0.02% bovine serum albumin, 0.02% polyvinylpyrrolidone, and about 0.1 mg/ml sheared, denatured salmon sperm DNA,
and/or

the wash medium contains about 3 x SSC, 25 mM phosphate buffer pH 7.1, and 20% deionized formamide and wherein the probe used is anyone of the probes of claim 8, the hybridization temperature being suitably adjusted to the range of about 40 to 58°C and/or the wash temperature to the range of about 40 to 58°C, and particularly, wherein said target sequence and the corresponding relevant hybridization temperature (HT) and wash temperature (WT), respectively, are as follows:

CAGGGCGACG TCACACTTGA CC

HT and/or WT: 45°C

GACGTCACAC TTGACCAAGA AC

HT and/or WT: 45°C

GCACAGTAGA TAGCTATAAC GAACGC

HT and/or WT: 40°C

TGCACAGTAG ATAGCAATAT CGAACGCA

HT and/or WT: 48°C

TTTTGTTCTTGGTCAAGGTGTGACGTCGCCCTGAATGGATTCTGTTCCATT

HT and/or WT: 58°C

GTCTGATGTT CTAGTCAACG GAATGTTAGG CAAA

HT and/or WT: 50°C

11. Kit for the detection in vitro of a large number, preferably all Neisseria meningitidis strains in a biological sample, with said kit containing: either

- at least one probe selected among any of those according to claim 8;
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a large number, preferably all strains of Neisseria meningitidis to be carried out;
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least two probes, targeting the same nucleic acid molecule, and of which at least one is specific for Neisseria meningitidis and which is selected from any one of the probes of claim 8,
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Neisseria meningitidis to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least one probe selected among any of those according to claim 4, which is fixed to a solid support,
- the primers needed for performing enzymatical amplification of the DNA and/or RNA containing the target sequence of the above-mentioned probe, when appropriate,
- the buffer or components necessary for producing the buffers enabling enzymatical amplification and/or enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Neisseria meningitidis to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate.

12. Probe for detecting one or more Haemophilus ducreyi strains, containing:

- either a sequence belonging to a nucleic acid selected from the following group of nucleic acids and which includes from 15 to the maximum number of nucleotides of the selected nucleic acid:

Group HDI1:

TTATTATGCG CGAGGCATAT TG	HDI1
CAATATGCCT CGCGCATAAT AA	HDI1IC
CAAUAUGCCU CGCGCAUAAU AA	HDI1ICR
UUAUUAUGCG CGAGGCAUAU UG	HDI1R

- or a variant sequence which distinguishes of any of the preceding sequences:
 - * either by addition to or removal from any of their respective extremities of one or several nucleotides;
 - * or changing within any of said sequences of one or more nucleotides;
 - * or both;

yet provided that in any of the above circumstances said probe still hybridizes with the same RNA or DNA target as the corresponding unmodified sequence.

13. Process for detecting Haemophilus ducreyi strains in a biological sample, wherein said process comprises contacting said biological sample - in which the nucleic acids (DNAs and/or RNAs) of the strains have been made accessible to hybridization, if need be, under suitable denaturation conditions, with said nucleic acid to be detected being possibly amplified using the polymerase chain reaction, with two primers, more preferably two more evolutionarily conserved primers, flanking the target sequence of the probe - with a probe according to any one of claim 12 under conditions enabling hybridization between the probe and complementary nucleic acids of the Haemophilus ducreyi strains, which may be present in the sample, and detecting the hybrids possibly formed, particularly with a probe hybridizing to both DNA and RNA of a Haemophilus ducreyi strain which may be present in the biological sample.

14. Process for detecting Haemophilus ducreyi, in a biological sample, according to anyone of claim 13, wherein:

the hybridization medium contains about 3 x SSC, (SSC = 0.15 M NaCl, 0.015 M sodium citrate, pH 7.0) about 25 mM of phosphate buffer pH 7.1, 20% deionized formamide, 0.02% Ficoll, 0.02% bovine serum albumin, 0.02% polyvinylpyrrolidone, and about 0.1 mg/ml sheared, denatured salmon sperm DNA,
and/or

the wash medium contains about 3 x SSC, 25 mM phosphate buffer pH 7.1, and 20% deionized formamide and wherein the probe used is anyone of the probes of claim 12, the hybridization temperature being suitable adjusted to the range of about 40°C and/or the wash temperatur

to the range of about 40°C, and particularly, wherein said target sequence and the corresponding relevant hybridization temperature (HT) and wash temperature (WT), respectively, are as follows:

CAATATGCCT CGCGCATAAT AA

HT and/or WT: 40 °C.

15. Kit for the detection in vitro of a large number, preferably all Haemophilus ducreyi strains in a biological sample, with said kit containing:

either

- at least one probe selected among any of those according to claim 12;
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a large number, preferably all strains of Haemophilus ducreyi to be carried out;
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least two probes, targeting the same nucleic acid molecule, and of which at least one is specific for Haemophilus ducreyi and which is selected from any one of the probes of claim 12,
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Haemophilus ducreyi to be carried out,
- means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least one probe selected among any of those according to claim 12, which is fixed to a solid support,
- the primers needed for performing enzymatical amplification of the DNA and/or RNA containing the

target sequence of the above-mentioned probe, when appropriate,

- the buffer or components necessary for producing the buffers enabling enzymatical amplification and/or enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Haemophilus ducreyi to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate.

16. Probe for detecting one or more Branhamella catarrhalis strains, containing:

- either a sequence belonging to a nucleic acid selected from the following group of nucleic acids and which includes from 15 to the maximum number of nucleotides of the selected nucleic acid:

Group BCII:

TTAAACATCT TACCAAAG	BCII
CTTTGGTAAG ATGTTTAA	BCI1IC
CUUUGGUAAAG AUGUUUAA	BCI1ICR
UUAAACAUCA UACCAAAG	BCI1R

Group BCII2:

TTGATGTTTA AACTTGCTTG GTGGA	BCI2
TCCACCAAGC AAGTTTAAAC ATCAA	BCI2IC
UCCACCAAGC AAGUUUAAAC AUCAA	BCI2ICR
UUGAUGUUUA AACUUGCUUG GUGGA	BCI2R

- or a variant sequence which distinguishes of any of the preceding sequences:
 - * either by addition to or removal from any of their respective extremities of one or several nucleotides;
 - * or changing within any of said sequences of one or more nucleotides;
 - * or both;

yet provided that in any of the above circumstances said probe still hybridizes with the same RNA or DNA target as the corresponding unmodified sequence.

17. Process for detecting Branhamella catarrhalis strains in a biological sample, wherein said process comprises contacting said biological sample - in which the nucleic acids (DNAs and/or RNAs) of the strains have been made accessible to hybridization, if need be, under suitable denaturation conditions, with said nucleic acid to be detected being possibly amplified using the polymerase chain reaction, with two primers, more preferably two more evolutionarily conserved primers, flanking the target sequence of the probe - with a probe according to any one of claim 16 under conditions enabling hybridization between the probe and complementary nucleic acids of the Branhamella catarrhalis strains, which may be present in the sample, and detecting the hybrids possibly formed, particularly with a probe hybridizing to both DNA and RNA of a Branhamella catarrhalis strain which may be present in the biological sample.

18. Process for detecting Branhamella catarrhalis, in a biological sample, according to claim 17, wherein: the hybridization medium contains about 3 x SSC, (SSC = 0.15 M NaCl, 0.015 M sodium citrate, pH 7.0) about 25 mM of phosphate buffer pH 7.1, 20% deionized formamide, 0.02% Ficoll, 0.02% bovine serum albumin, 0.02% polyvinylpyrrolidone, and about 0.1 mg/ml sheared, denatured salmon sperm DNA,
and/or
the wash medium contains about 3 x SSC, 25 mM phosphate buffer pH 7.1, and 20% deionized formamide and wherein the probe used is anyone of the probes of claim 16, the hybridization temperature being suitable adjusted to the range of about 30°C to 42°C and/or the wash temperature to the range of about 30°C to 42°C, and

particularly, wherein said target sequence and the corresponding relevant hybridization temperature (HT) and wash temperature (WT), respectively, are as follows:

CTTTGGTAAG ATGTTTAA

HT and/or WT: 30°C

TCCACCAAGC AAGTTAAC ATCAA

HT and/or WT: 42°C

19. Kit for the detection in vitro of a large number, preferably all Branhamella catarrhalis strains in a biological sample, with said kit containing: either

- at least one probe selected among any of those according to claim 16;
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a large number, preferably all strains of Branhamella catarrhalis to be carried out;
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least two probes, targeting the same nucleic acid molecule, and of which at least one is specific for Branhamella catarrhalis and which is selected from any one of the probes of claim 16,
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Branhamella catarrhalis to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least one probe selected among any of those according to claim 16, which is fixed to a solid support,

- the primers needed for performing enzymatical amplification of the DNA and/or RNA containing the target sequence of the above-mentioned probe, when appropriate,
- the buffer or components necessary for producing the buffers enabling enzymatical amplification and/or enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Branhamella catarrhalis to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate.

20. Probe for detecting one or more Bordetella pertussis strains, containing:

- either a sequence belonging to a nucleic acid selected from the following group of nucleic acids and which includes from 15 to the maximum number of nucleotides of the selected nucleic acid:

Group BPI1:

CCACACCCAT CCTCTGGACA GGCTT	BPI1
AAGCCTGTCC AGAGGGATGGG TGTGG	BPI1IC
AAGCCUGUCC AGAGGAUGGG UGUGG	BPI1ICR
CCACACCCAU CCUCUGGACA GGCUU	BPI1R

- or a variant sequence which distinguishes of any of the preceding sequences:
 - * either by addition to or removal from any of their respective extremities of one or several nucleotides;
 - * or changing within any of said sequences of one or more nucleotides;
 - * or both;

yet provided that in any of the above circumstances said probe still hybridizes with the same RNA or DNA target as the corresponding unmodified sequence.

21. Process for detecting Bordetella pertussis strains in a biological sample, wherein said process comprises contacting said biological sample - in which the nucleic acids (DNAs and/or RNAs) of the strains have been made accessible to hybridization, if need be, under suitable denaturation conditions, with said nucleic acid to be detected being possibly amplified using the polymerase chain reaction, with two primers, more preferably two more evolutionarily conserved primers, flanking the target sequence of the probe - with a probe according to any one of claim 20 under conditions enabling hybridization between the probe and complementary nucleic acids of the Bordetella pertussis strains, which may be present in the sample, and detecting the hybrids possibly formed, particularly with a probe hybridizing to both DNA and RNA of a Bordetella pertussis strain which may be present in the biological sample.

22. Process for detecting Bordetella pertussis, in a biological sample, according to claim 21, wherein: the hybridization medium contains about 3 x SSC, (SSC = 0.15 M NaCl, 0.015 M sodium citrate, pH 7.0) about 25 mM of phosphate buffer pH 7.1, 20% deionized formamide, 0.02% Ficoll, 0.02% bovine serum albumin, 0.02% polyvinylpyrrolidone, and about 0.1 mg/ml sheared, denatured salmon sperm DNA, and/or

the wash medium contains about 3 x SSC, 25 mM phosphate buffer pH 7.1, and 20% deionized formamide and wherein the probe used is anyone of the probes of claim 20, the hybridization temperature being suitable adjusted to the range of about 55°C and/or the wash temperature to the range of about 55°C, and particularly, wherein said target sequence and the corresponding relevant hybridization temperature (HT) and wash temperature (WT), respectively, are as follows:

AAGCCTGTCC AGAGGATGGG TGTGG

HT and/or WT: 55°C.

23. Kit for the detection in vitro of a large number, preferably all Bordetella pertussis strains in a biological sample, with said kit containing:

either

- at least one probe selected among any of those according to claim 20;
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a large number, preferably all strains of Bordetella pertussis to be carried out;
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least two probes, targeting the same nucleic acid molecule, and of which at least one is specific for Bordetella pertussis and which is selected from any one of the probes of claim 20,
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Bordetella pertussis to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least one probe selected among any of those according to claim 20, which is fixed to a solid support,
- the primers needed for performing enzymatical amplification of the DNA and/or RNA containing the target sequence of the above-mentioned probe, when appropriate,
- the buffer or components necessary for producing the buffers enabling enzymatical amplification

and/or enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Bordetella pertussis to be carried out,

- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate.

24. Probe for detecting one or more Haemophilus influenzae strains, containing:

- either a sequence belonging to a nucleic acid selected from the following group of nucleic acids and which includes from 15 to the maximum number of nucleotides of the selected nucleic acid:

Group HII1:

ACGCATCAAA TTGACCGCAC TT	HII1
AAGTGC GGTC AATTTGATGC GT	HII1IC
AAGUGC GGUC AAUUUGAUGC GU	HII1ICR
ACGCAUCAAA UUGACCGCAC UU	HII1R

Group HII2:

ACTTTGAAGT GAAAAC TAA AG	HII2
CTTTAAGTTT TCAC TCAAA GT	HII2IC
CUUUUAGUUU UCACUUCAAA GU	HII2ICR
ACUUUGAAGU GAAAACUUAA AG	HII2R

- or a variant sequence which distinguishes of any of the preceding sequences:

- * either by addition to or removal from any of their respective extremities of one or several nucleotides;
- * or changing within any of said sequences of one or more nucleotides;
- * or both;

yet provided that in any of the above circumstances said probe still hybridizes with the same RNA or DNA target as the corresponding unmodified sequence.

25. Process for detecting Haemophilus influenzae strains in a biological sample, wherein said process

comprises contacting said biological sample - in which the nucleic acids (DNAs and/or RNAs) of the strains have been made accessible to hybridization, if need be, under suitable denaturation conditions, with said nucleic acid to be detected being possibly amplified using the polymerase chain reaction, with two primers, more preferably two more evolutionarily conserved primers, flanking the target sequence of the probe - with a probe according to anyone of claim 24 under conditions enabling hybridization between the probe and complementary nucleic acids of the Haemophilus influenzae strains, which may be present in the sample, and detecting the hybrids possibly formed, particularly with a probe hybridizing to both DNA and RNA of a Haemophilus influenzae strain which may be present in the biological sample.

26. Process for detecting Haemophilus influenzae, in a biological sample, according to claim 25, wherein: the hybridization medium contains about 3 x SSC, (SSC = 0.15 M NaCl, 0.015 M sodium citrate, pH 7.0) about 25 mM of phosphate buffer pH 7.1, 20% deionized formamide, 0.02% Ficoll, 0.02% bovine serum albumin, 0.02% polyvinylpyrrolidone, and about 0.1 mg/ml sheared, denatured salmon sperm DNA,
and/or

the wash medium contains about 3 x SSC, 25 mM phosphate buffer pH 7.1, and 20% deionized formamide and wherein the probe used is anyone of the probes of claim 24, the hybridization temperature being suitable adjusted to the range of about 35°C to 55°C and/or the wash temperature to the range of about 35°C to 55°C, and particularly wherein said target sequence and the corresponding relevant hybridization temperature (HT) and wash temperature (WT), respectively, are as follows:

AAGTGC~~GG~~TC AATTTGATGC GT

HT and/or WT: 55°C

CTTTAAGTTT TCACCTCAAA GT

HT and/or WT: 35°C

27. Kit for the detection in vitro of a large number, preferably all Haemophilus influenzae strains in a biological sample, with said kit containing:

either

- at least one probe selected among any of those according to claim 24,
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a large number, preferably all strains of Haemophilus influenzae to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least two probes, targeting the same nucleic acid molecule, and of which at least one is specific for Haemophilus influenzae and which is selected from any one of the probes of claim 24,
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Haemophilus influenzae to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least one probe selected among any of those according to claim 24, which is fixed to a solid support,
- the primers needed for performing enzymatical amplification of the DNA and/or RNA containing the target sequence of the above-mentioned probe, when appropriate,

- the buffer or components necessary for producing the buffers enabling enzymatical amplification and/or enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Haemophilus influenzae to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate.

28. Probe for detecting one or more Streptococcus pneumoniae strains, containing:

- either a sequence belonging to a nucleic acid selected from the following groups of nucleic acids and which includes from 15 to the maximum number of nucleotides of the selected nucleic acid:

Group SPI1:

GTGAGAGATC ACCAAGTAAT GCA	SPI1
TGCATTACTT GGTGATCTCT CAC	SPI1IC
UGCAUUACUU GGUGAUCUCU CAC	SPI1ICR
GUGAGAGAUC ACCAAGUAAU GCA	SPI1R

Group SPI2

AGGAACTGCG CATTGGTCTT	SPI2
AAGACCAATG CGCAGTTCT	SPI2IC
AAGACCAAUG CGCAGUUCCU	SPI2ICR
AGGAACUGCG CAUUGGUCUU	SPI2R

Group SPI3

GAGTTTATGA CTGAAAGGTC AGAA	SPI3
TTCTGACCTT TCAGTCATAA ACTC	SPI3IC
UUCUGACCUU UCAGUCAUAA ACUC	SPI3ICR
GAGUUUAUGA CUGAAAGGUC AGAA	SPI3R

- or a variant sequence which distinguishes of any of the preceding sequences:

- * either by addition to or removal from any of their respective extremities of one or several nucleotides;
- * or changing within any of said sequences of one or more nucleotides;
- * or both;

yet provided that in any of the above circumstances said probe still hybridizes with the same RNA or DNA target as the corresponding unmodified sequence.

29. Process for detecting Streptococcus pneumoniae strains in a biological sample, wherein said process comprises contacting said biological sample - in which the nucleic acids (DNAs and/or RNAs) of the strains have been made accessible to hybridization, if need be, under suitable denaturation conditions, with said nucleic acid to be detected being possibly amplified using the polymerase chain reaction, with two primers, more preferably two more evolutionarily conserved primers, flanking the target sequence of the probe - with a probe according to anyone of claim 28 under conditions enabling hybridization between the probe and complementary nucleic acids of the Streptococcus pneumoniae strains, which may be present in the sample, and detecting the hybrids possibly formed, particularly with a probe hybridizing to both DNA and RNA of a Streptococcus pneumoniae strain which may be present in the biological sample.

30. Process for detecting Streptococcus pneumoniae, in a biological sample, according to claim 29, wherein: the hybridization medium contains about 3 x SSC, (SSC = 0.15 M NaCl, 0.015 M sodium citrate, pH 7.0) about 25 mM of phosphate buffer pH 7.1, 20% deionized formamide, 0.02% Ficoll, 0.02% bovine serum albumin, 0.02% polyvinylpyrrolidone, and about 0.1 mg/ml sheared, denatured salmon sperm DNA, and/or

the wash medium contains about 3 x SSC, 25 mM phosphate buffer pH 7.1, and 20% deionized formamide and wherein the probe used is anyone of the probes of claim 28, the hybridization temperature being suitable adjusted to the range of about 45°C and/or the wash temperature to the range of about 45°C, and particularly wherein said target sequence and the corresponding relevant hybridization temperature (HT) and wash temperature (WT), respectively, are as follows:

TGCATTACTT GGTGATCTCT CAC

HT and/or WT: 45°C

AAGACCAATG CGCAGTTCCCT

HT and/or WT: 45°C

TTCTGACCTT TCAGTCATAA ACTG

HT and/or WT: 45°C

31. Kit for the detection in vitro of a large number, preferably all Streptococcus pneumoniae strains in a biological sample, with said kit containing: either

- at least one probe selected among any of those according to claim 28;
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a large number, preferably all strains of Streptococcus pneumoniae to be carried out;
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least two probes, targeting the same nucleic acid molecule, and of which at least one is specific for Streptococcus pneumoniae and which is selected from any one of the probes of claim 28,
- the buffer or components necessary for producing the buffer enabling hybridization reaction between

these probes and the DNAs and/or RNAs of a strain of Streptococcus pneumoniae to be carried out,

- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least one probe selected among any of those according to claim 28, which is fixed to a solid support,
- the primers needed for performing enzymatical amplification of the DNA and/or RNA containing the target sequence of the above-mentioned probe, when appropriate,
- the buffers or components necessary for producing the buffers enabling enzymatical amplification and/or enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Streptococcus pneumoniae to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate.

32. Probe for detecting one or more Streptococcus agalactiae strains, containing:

- either a sequence belonging to a nucleic acid selected from the following groups of nucleic acids and which includes from 15 to the maximum number of nucleotides of the selected nucleic acid:

Group SAI1:

AATCGAAAGG TTCAAATTGT T
 AACAAATTGA ACCTTTCGAT T
 AACAAUUUGA ACCUUUCGAU U
 AAUCGAAAGG UUCAAAUUGU U

SAI1
 SAI1IC
 SAI1ICR
 SAI1R

Group SAI2:

GGAAACCTGC CATTGCGTC TT
 AAGACGCCAA TGGCAGGTTT CC

SAI2
 SAI2IC

AAGACGCAAA UGGCAGGUUU CC
GGAAACCUGC CAUUUGCGUC UU

SAI2ICR
SAI2R

Group SAI3:

TCCACGATCT AGAAATAGAT TGTAGAA
TTCTACAATC TATTCTAGA TCGTGGAA
UUCUACAAUC UAUUUCUAGA UCGUGGAA
UCCACGAUCU AGAAAUAAGAU UGUAGAA

SAI3
SAI3IC
SAI3ICR
SAI3R

Group SAI4:

TCTAGTTTA AAGAAACTAG GTT
AACCTAGTTT CTTTAAAAC AGA
AACCUAGUUU CUUUAAAACU AGA
UCUAGUUUUA AAGAAACUAG GUU

SAI4
SAI4IC
SAI4ICR
SAI4R

- or a variant sequence which distinguishes of any of the preceding sequences:

- * either by addition to or removal from any of their respective extremities of one or several nucleotides;
- * or changing within any of said sequences of one or more nucleotides;
- * or both;

yet provided that in any of the above circumstances said probe still hybridizes with the same RNA or DNA target as the corresponding unmodified sequence.

33. Process for detecting Streptococcus agalactiae strains in a biological sample, wherein said process comprises contacting said biological sample - in which the nucleic acids (DNAs and/or RNAs) of the strains have been made accessible to hybridization, if need be, under suitable denaturation conditions, with said nucleic acid to be detected being possibly amplified using the polymerase chain reaction, with two primers, more preferably two more evolutionarily conserved primers, flanking the target sequence of the probe - with a probe according to anyone of claim 32 under

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conditions enabling hybridization between the probe and complementary nucleic acids of the Streptococcus agalactiae strains, which may be present in the sample, and detecting the hybrids possibly formed, particularly with a probe hybridizing to both DNA and RNA of a Streptococcus agalactiae strain which may be present in the biological sample.

34. Process for detecting Streptococcus agalactiae, in a biological sample, according to claim 33, wherein:

the hybridization medium contains about 3 x SSC, (SSC = 0.15 M NaCl, 0.015 M sodium citrate, pH 7.0) about 25 mM of phosphate buffer pH 7.1, 20% deionized formamide, 0.02% Ficoll, 0.02% bovine serum albumin, 0.02% polyvinylpyrrolidone, and about 0.1 mg/ml sheared, denatured salmon sperm DNA,

and/or

the wash medium contains about 3 x SSC, 25 mM phosphate buffer pH 7.1, and 20% deionized formamide and wherein the probe used is anyone of the probes of claim 32, the hybridization temperature being suitable adjusted to the range of about 35°C to 45°C and/or the wash temperature to the range of about 35°C to 45°C, and particularly wherein said target sequence and the corresponding relevant hybridization temperature (HT) and wash temperature (WT), respectively, are as follows:

AACAATTGAT ACCTTCGAT T

HT and/or WT: 35°C

AAGACGCAAA TGGCAGGTCC

HT and/or WT: 45°C

TTCTACAATC TATTTCTAGA TCGTGGAT

HT and/or WT: 45°C

AACCTAGTTT CTTTAAACT AGA

HT and/or WT: 37°C

35. Kit for the detection in vitro of a large number, preferably all Streptococcus agalactiae strains in a biological sample, with said kit containing:
either

- at least one probe selected among any of those according to claim 32;
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a large number, preferably all strains of Streptococcus agalactiae to be carried out;
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,
or
- at least two probes, targeting the same nucleic acid molecule, and of which at least one is specific for Streptococcus agalactiae and which is selected from any one of the probes of claim 32,
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Streptococcus agalactiae to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,
or
- at least one probe selected among any of those according to claim 32, which is fixed to a solid support,
- the primers needed for performing enzymatical amplification of the DNA and/or RNA containing the target sequence of the above-mentioned probe, when appropriate,
- the buffers or components necessary for producing the buffers enabling enzymatical amplification and/or enabling hybridization reaction between

these probes and the DNAs and/or RNAs of a strain of Streptococcus agalactiae to be carried out,

- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate.

36. Probe for detecting one or more Campylobacter jejuni and Campylobacter coli strains, containing a sequence from 15 to the maximum number of nucleotides derived from the 16S-23S rRNA spacer sequence shown in Fig. 10 or its complement provided that the probe, at the appropriate conditions, hybridizes exclusively with DNA and/or RNA from Campylobacter jejuni and Campylobacter coli strains and not with DNA and/or RNA from other organisms.

37. Process for detecting Campylobacter jejuni and Campylobacter coli strains in a biological sample, wherein said process comprises contacting said biological sample - in which the nucleic acids (DNAs and/or RNAs) of the strains have been made accessible to hybridization, if need be, under suitable denaturation conditions, with said nucleic acid to be detected being possibly amplified using the polymerase chain reaction, with two primers, more preferably two more evolutionarily conserved primers, flanking the target sequence of the probe - with a probe according to anyone of claim 36 under conditions enabling hybridization between the probe and complementary nucleic acids of the Campylobacter jejuni and Campylobacter coli strains, which may be present in the sample, and detecting the hybrids possibly formed, particularly with a probe hybridizing to both DNA and RNA of a Campylobacter jejuni or Campylobacter coli strain which may be present in the biological sample.

38. Kit for the detection in vitro of a large number, preferably all Campylobacter jejuni and Campylobacter coli strains in a biological sample, with said kit containing:

either

- at least one probe selected among any of those according to claim 36;
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a large number, preferably all strains of Campylobacter jejuni or Campylobacter coli to be carried out;
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least two probes, targeting the same nucleic acid molecule, and of which at least one is specific for Campylobacter jejuni and Campylobacter coli and which is selected from any one of the probes of claim 36,
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Campylobacter jejuni or Campylobacter coli to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least one probe selected among any of those according to claim 36, which is fixed to a solid support,
- the primers needed for performing enzymatical amplification of the DNA and/or RNA containing the target sequence of the above-mentioned probe, when appropriate,
- the buffers or components necessary for producing the buffers enabling enzymatical amplification and/or enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain

of Campylobacter jejuni or Campylobacter coli to be carried out,

- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate.

39. Process for the in vitro detection of one microorganism or to the simultaneous in vitro detection of several microorganisms contained in a biological sample using anyone of the probes according to claims 1 to 4, 8, 12, 16, 20, 24, 28, 32 and 36, and specific for the microorganism(s) to be detected wherein the DNA and/or RNA present in the biological sample (and comprising the target sequence) is labeled, preferably using enzymatic amplification with at least one set of primers flanking the probe region, and wherein said biological sample is contacted with a membrane on which one or more oligonucleotide probes are dot spotted on a known location, in a medium enabling specific hybridization of the amplified target sequence and the probes on the membrane and wherein the hybrids resulting from the hybridizations are detected by appropriate means.

40. Kit for the in vitro detection of one microorganism or for the simultaneous in vitro detection of several microorganisms contained in a biological sample, with said kit containing:

- at least one of the probes according to claims 1 to 4, 8, 12, 16, 20, 24, 28, 32 and 36, and specific for the microorganism(s) to be detected, which is dot spotted to a membrane,
- the primers needed for performing enzymatical amplification of the DNA and/or RNA containing the target sequence of the above-mentioned probe, when appropriate,
- the buffers or components necessary for producing the buffers enabling enzymatic amplification and/or enabling hybridization reaction between

these probes and the DNAs and/or RNAs of a microorganism or microorganisms which are to be detected to be carried out,

- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate.